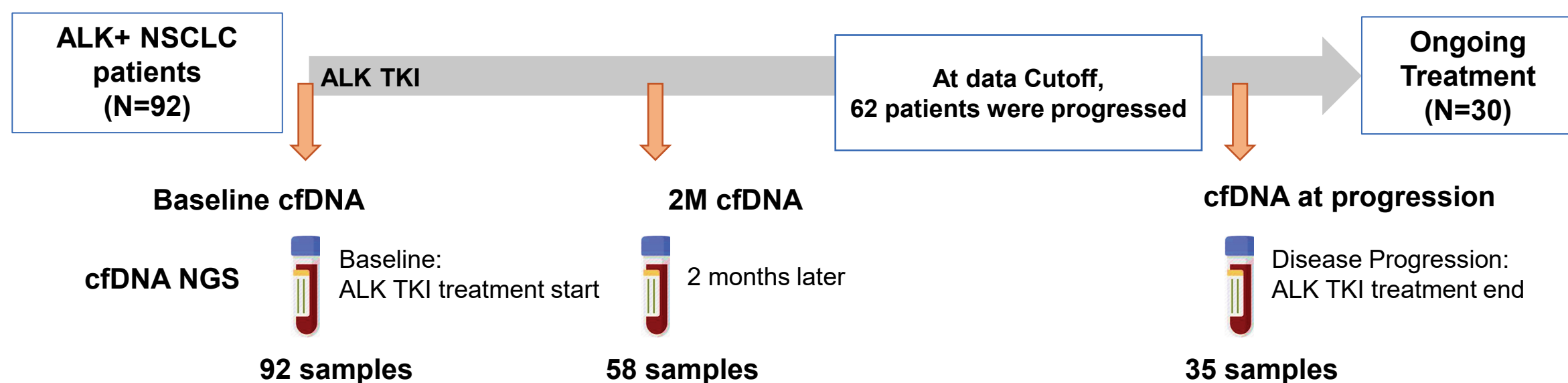


Supplementary figure 1

A

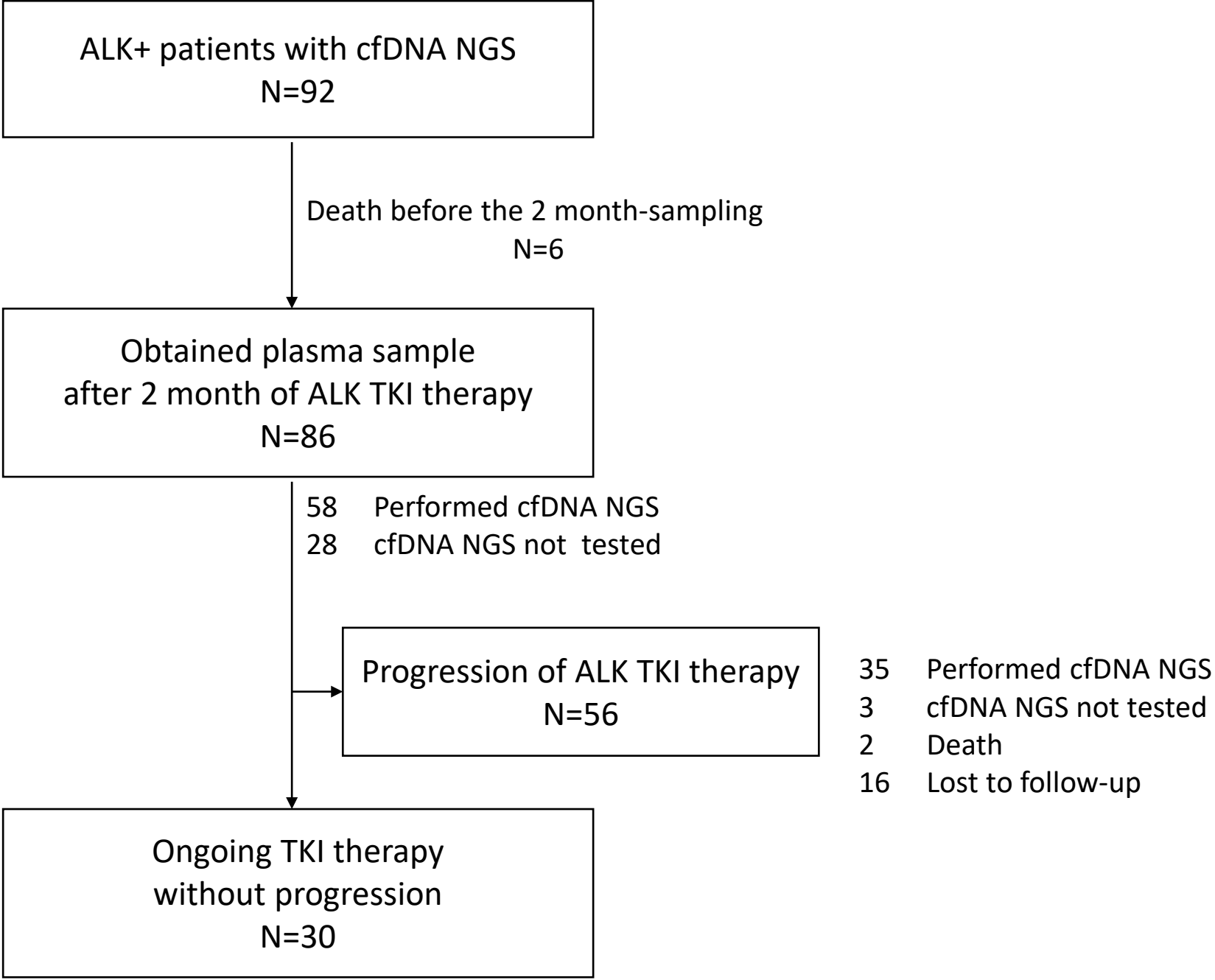


B

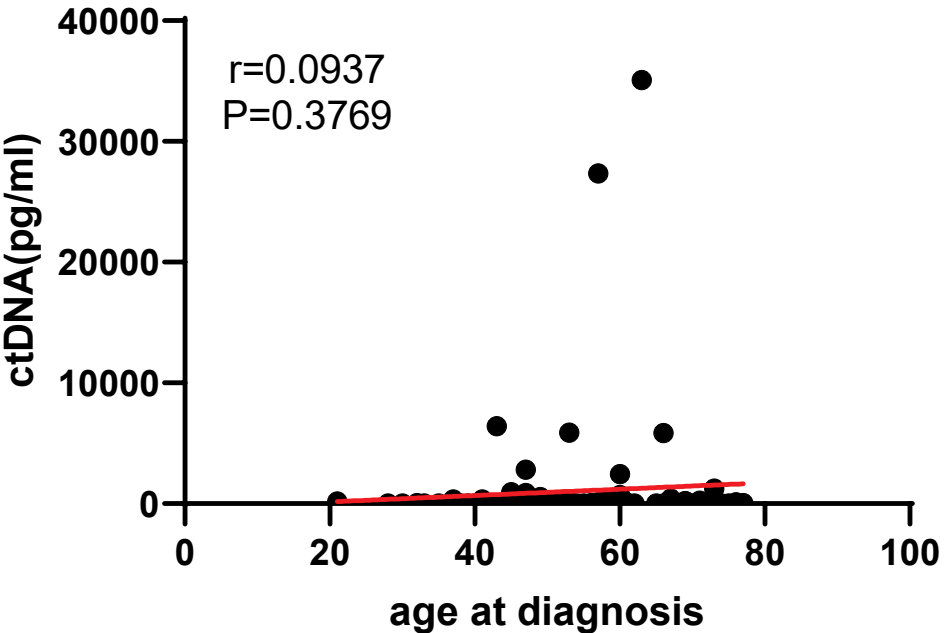
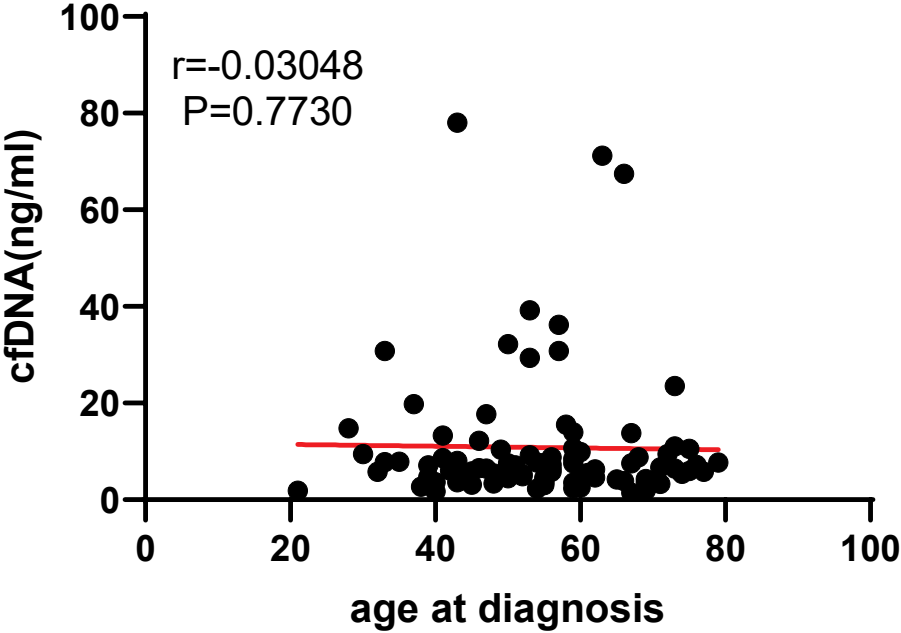
Point Mutations (SNVs) (73 Genes)						Indels (23 Genes)		Amplifications (18 Genes)		Fusions (6 Genes)
AKT1	ALK	APC	AR	ARAF	ARID1A	ATM	APC	AR	BRAF	ALK
ATM	BRAF	BRCA1	BRCA2	CCND1	CCND2	ARID1A	BRCA1	CCND1	CCND2	FGFR2
CCNE1	CDH1	CDK4	CDK6	CDKN2A	CTNNB1	BRCA2	CDH1	CCNE1	CDK4	FGFR3
DDR2	EGFR	ERBB2 (HER2)	ESR1	EZH2	FBXW7	CDKN2A	EGFR	CDK6	EGFR	NTRK1
FGFR1	FGFR2	FGFR3	GATA3	GNA11	GNAQ	ERBB2	GATA3	ERBB2	FGFR1	RET
GNAS	HNF1A	HRAS	IDH1	IDH2	JAK2	KIT	MET	FGFR2	KIT	ROS1
JAK3	KIT	KRAS	MAP2K1/MEK1	MAP2K2/MEK2	MAPK1/ERK2	MLH1	MTOR	KRAS	MET	
MAPK3/ERK1	MET	MLH1	MPL	MTOR	MYC	NF1	PDGFRA	MYC	PDGFRA	
NF1	NPM1	NOTCH1	NFE2L2	NRAS	NTRK1	PTEN	RB1	PIK3CA	RAF1	
NTRK3	PDGFRA	PIK3CA	PTEN	PTPN11	RAF1	SMAD4	STK11			
RB1	RET	RHEB	RHOA	RIT1	ROS1	TP53	TSC1			
SMAD4	SMO	STK11	TERT†	TP53	SC1	VHL				
VHL										

*Exons selected to maximize detection of known somatic mutations / † Includes TERT promoter region

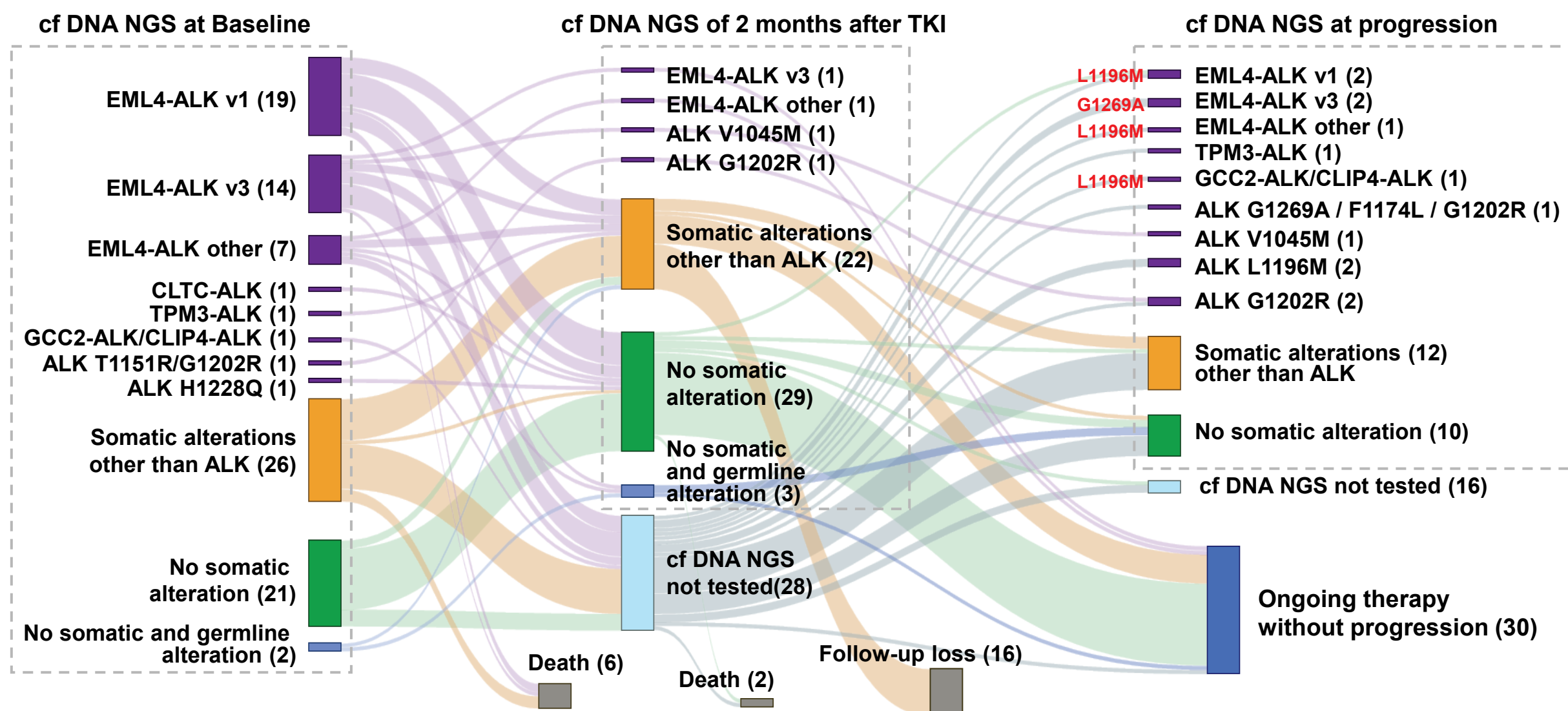
Supplementary figure 2



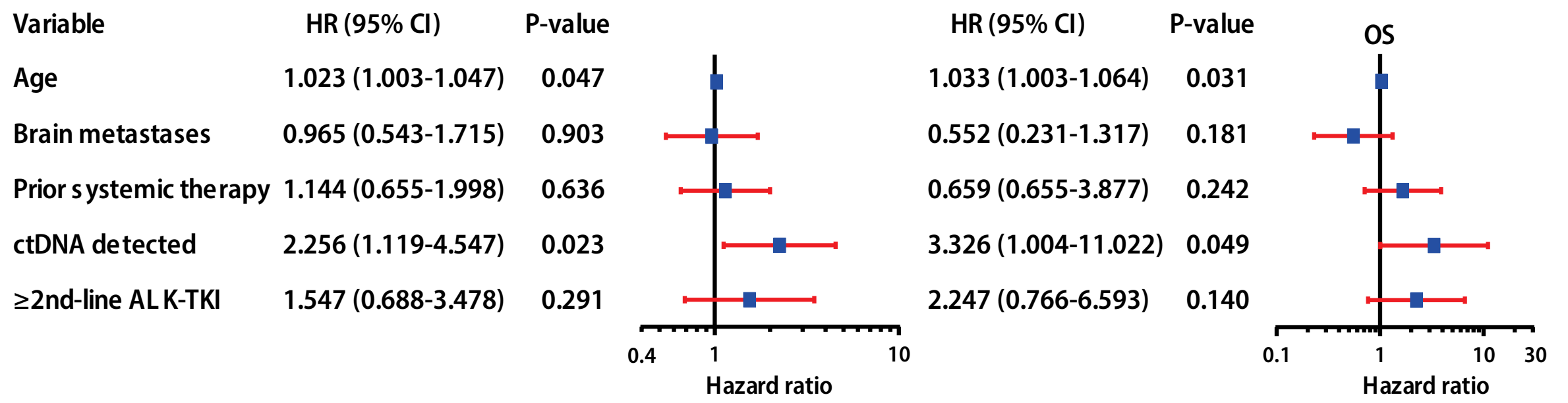
Supplementary figure 3



Supplementary figure 4



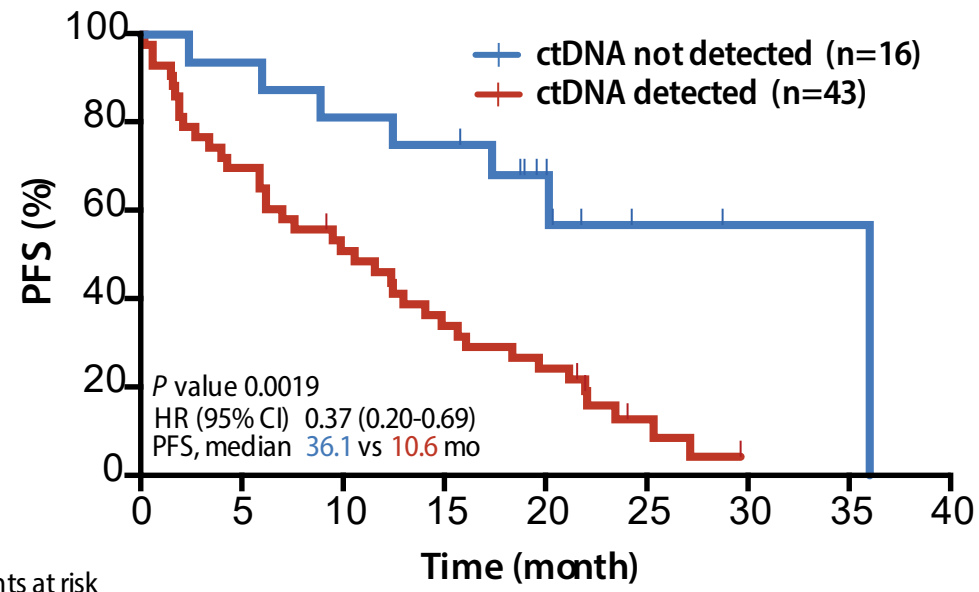
Supplementary figure 5



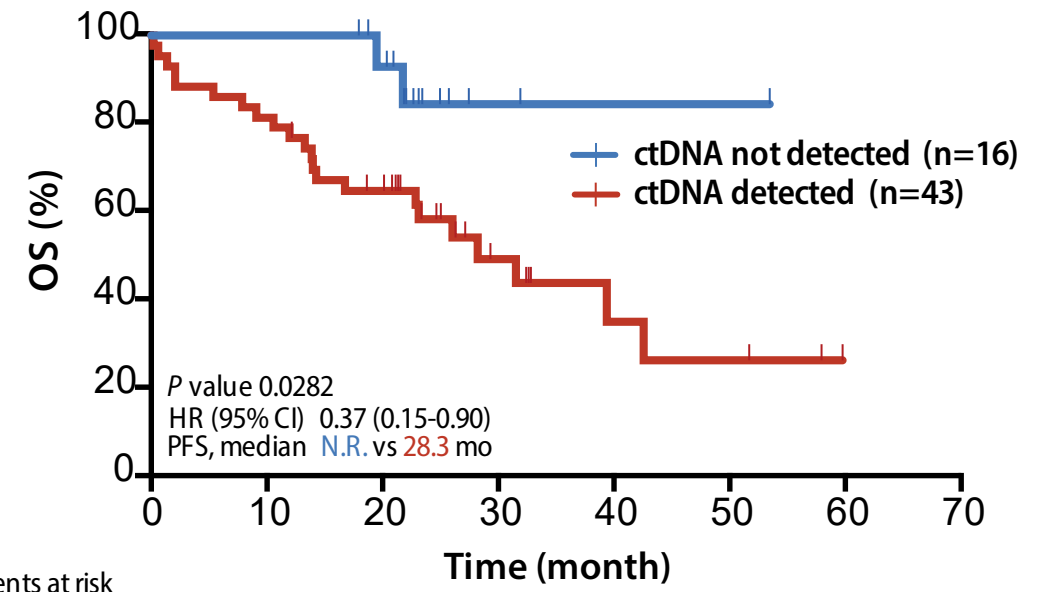
Supplementary figure 6

A

First-line Crizotinib subgroup



First-line Crizotinib subgroup



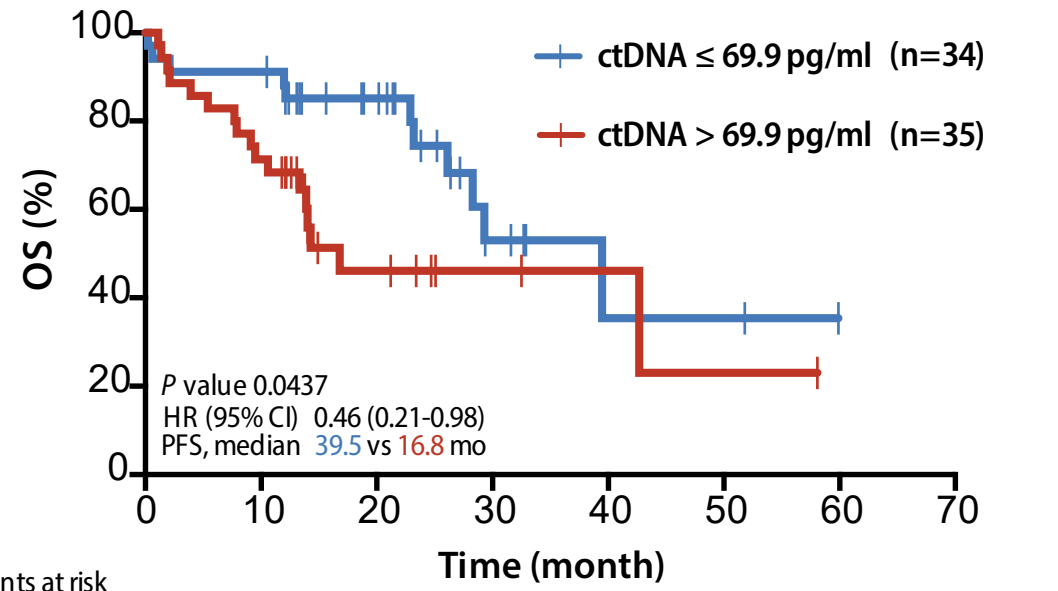
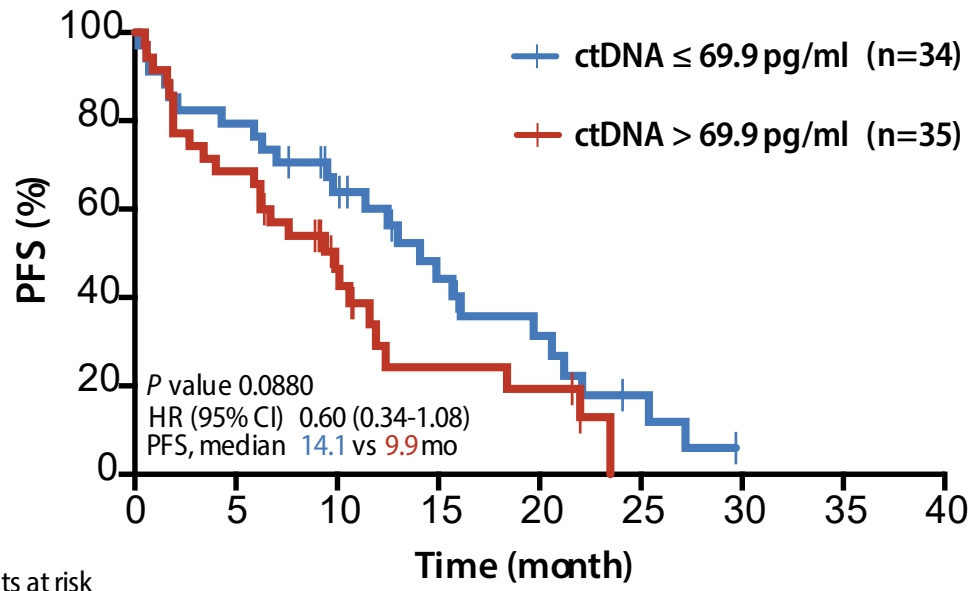
Patients at risk

ctDNA not detected	16	15	13	12	7	2	1	1	0
ctDNA detected	43	30	21	14	10	3	0	0	0

Patients at risk

ctDNA not detected	16	16	13	2	1	1	0	0
ctDNA detected	43	35	26	9	4	3	0	0

B



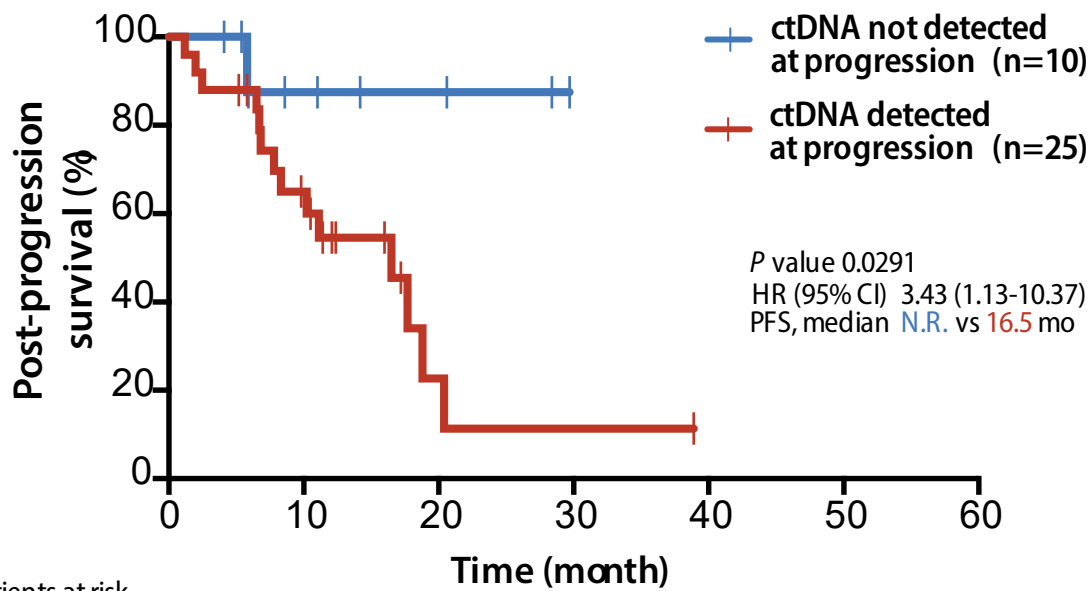
Patients at risk

ctDNA ≤ 69.9 pg/ml	34	27	19	11	7	3	0	0	0
ctDNA > 69.9 pg/ml	35	24	12	5	4	0	0	0	

Patients at risk

ctDNA ≤ 69.9 pg/ml	34	31	20	6	3	2	0	0
ctDNA > 69.9 pg/ml	35	24	9	3	2	1	0	0

C

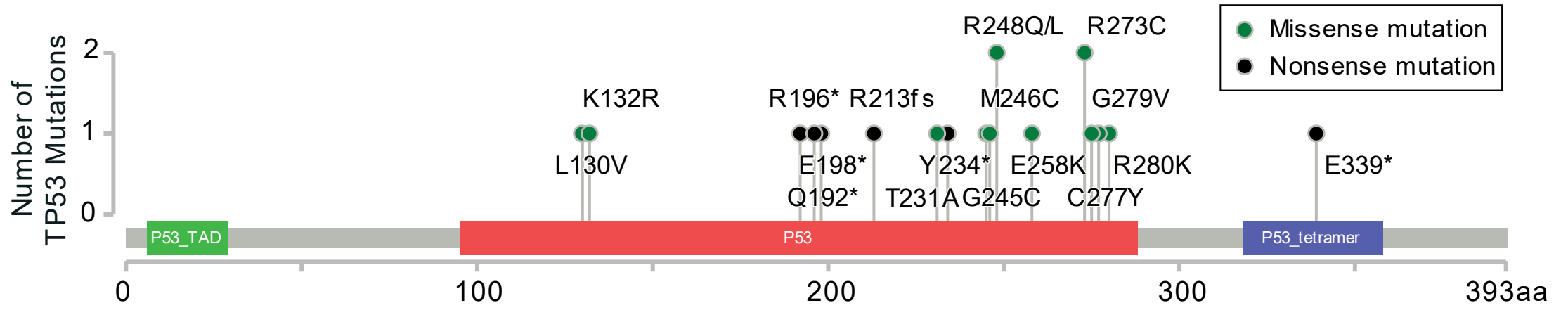


Patients at risk

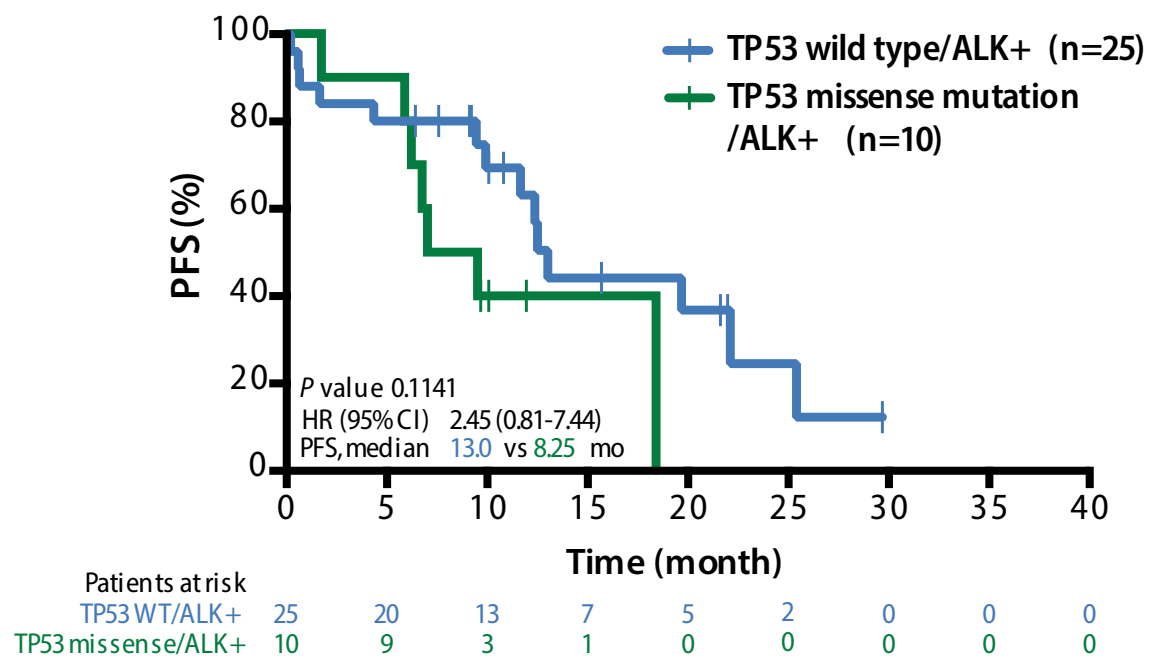
ctDNA Not detected	10	5	3	0	0	0	0
ctDNA detected	16	13	2	1	0	0	0

Supplementary figure 7

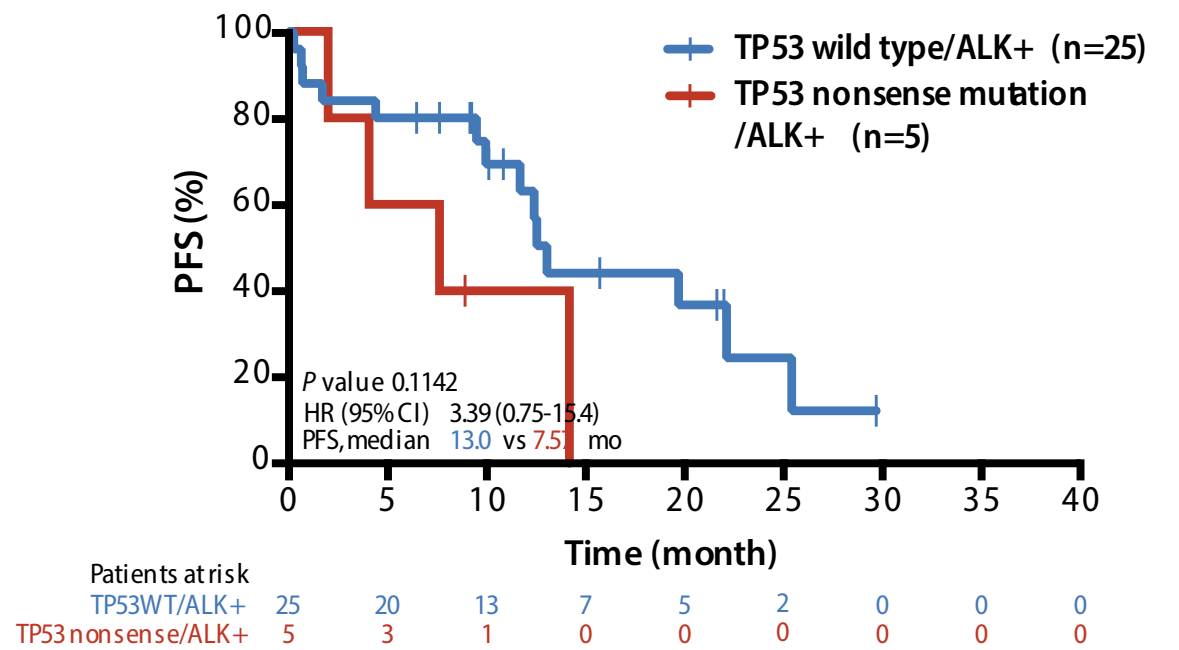
A



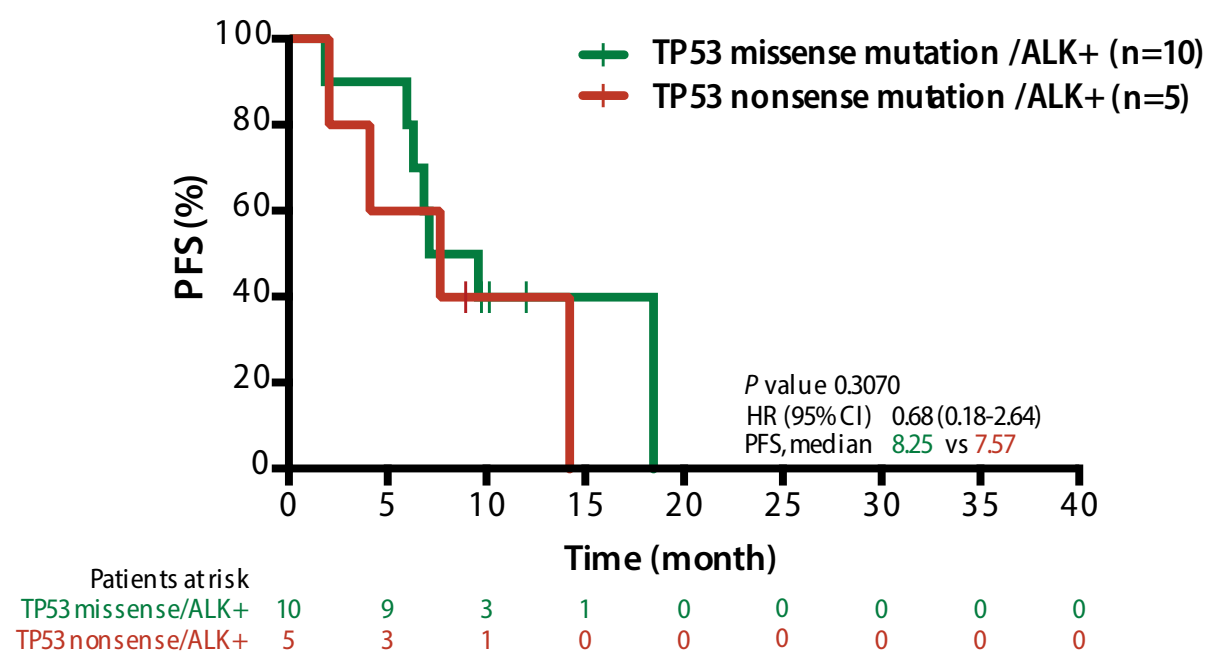
B



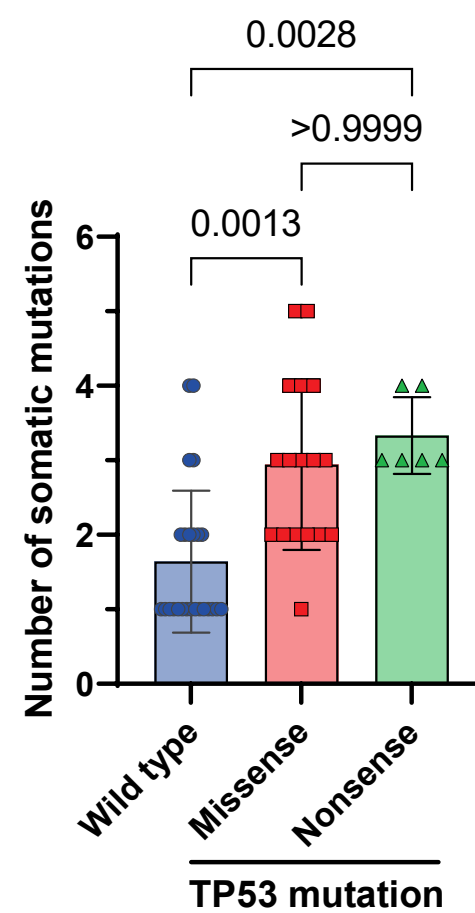
C



D



E



Supplementary figure 8

